

002201" 50/86960

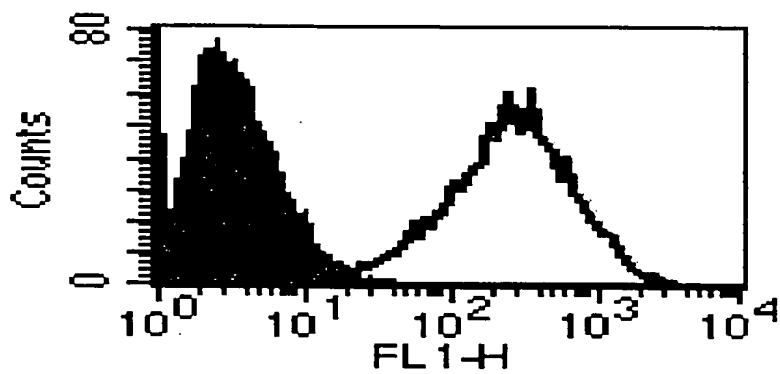


FIG. 1

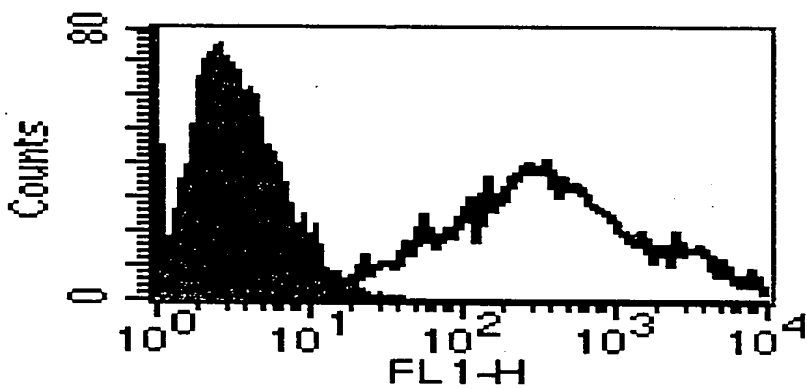


FIG. 2

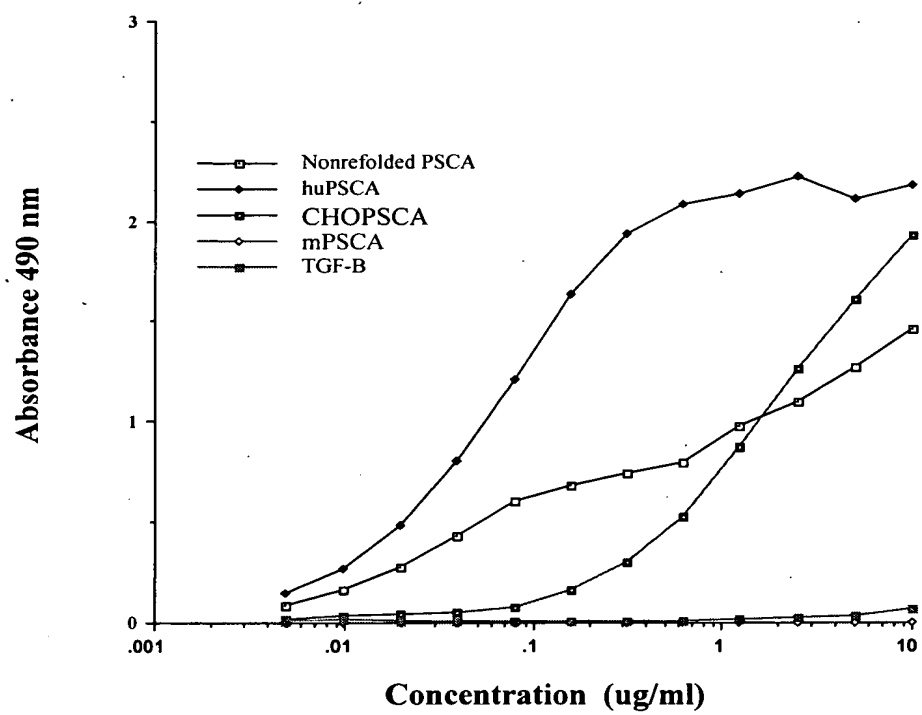


FIG. 3

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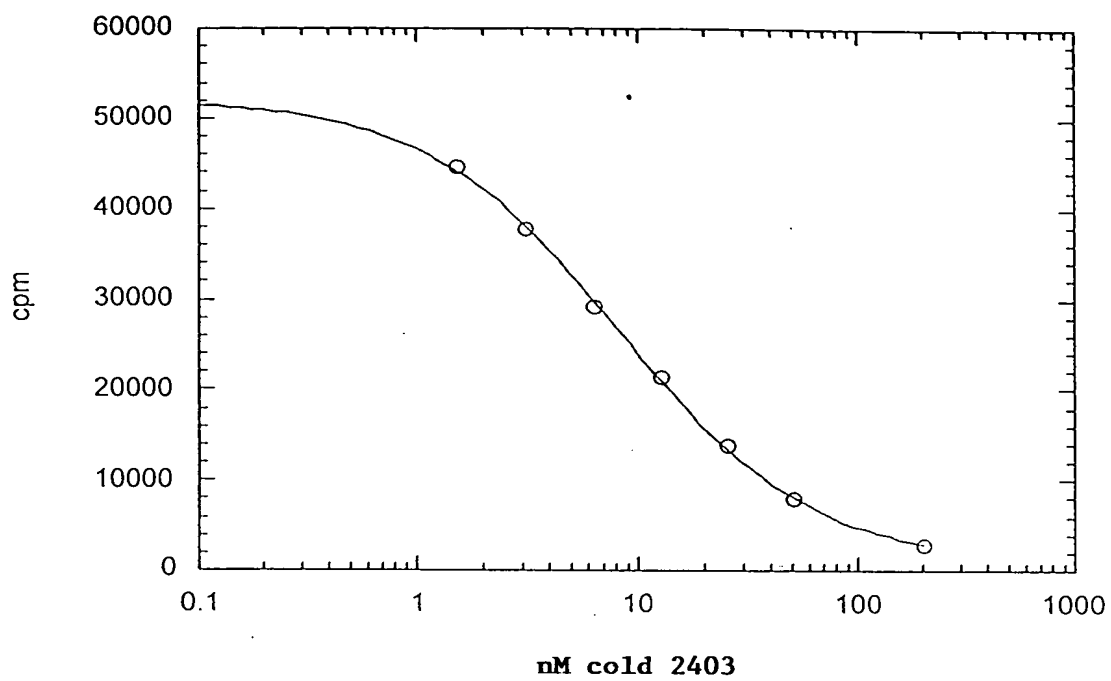


FIG. 4

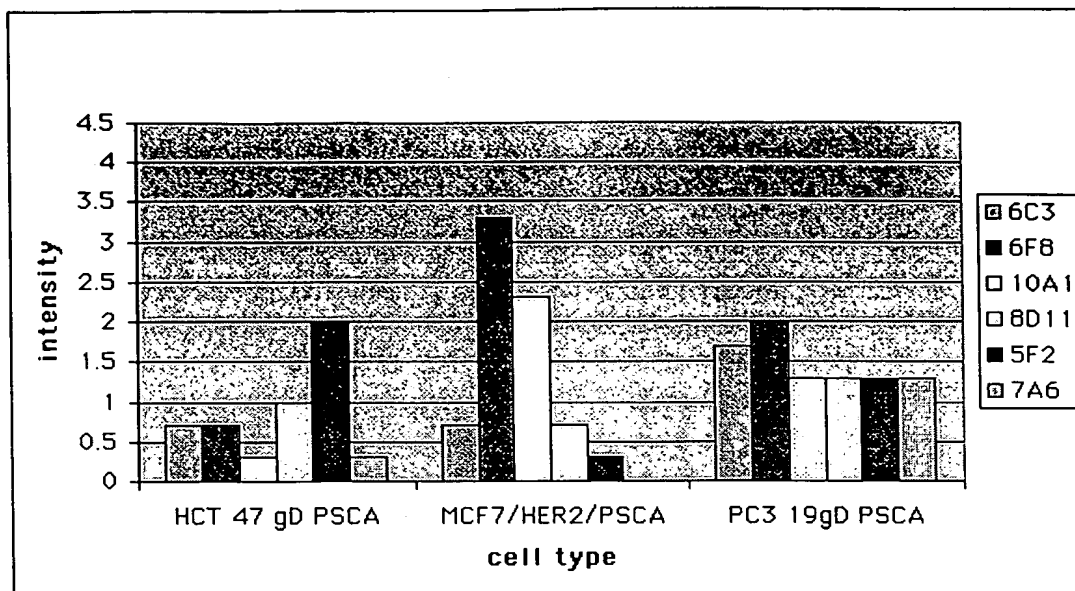


Fig. 5

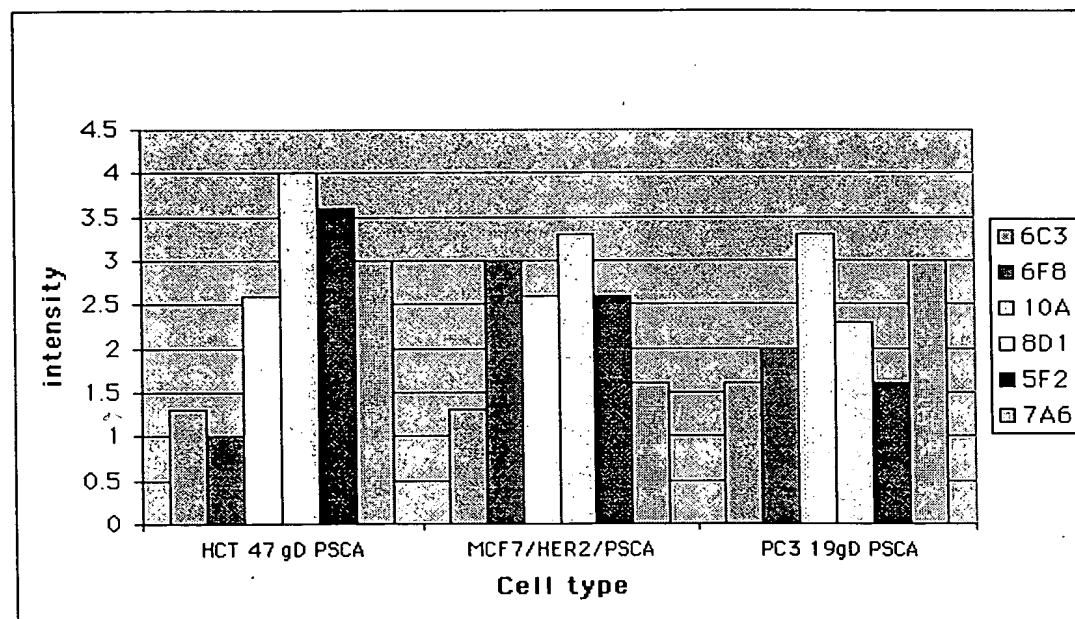


Fig. 6

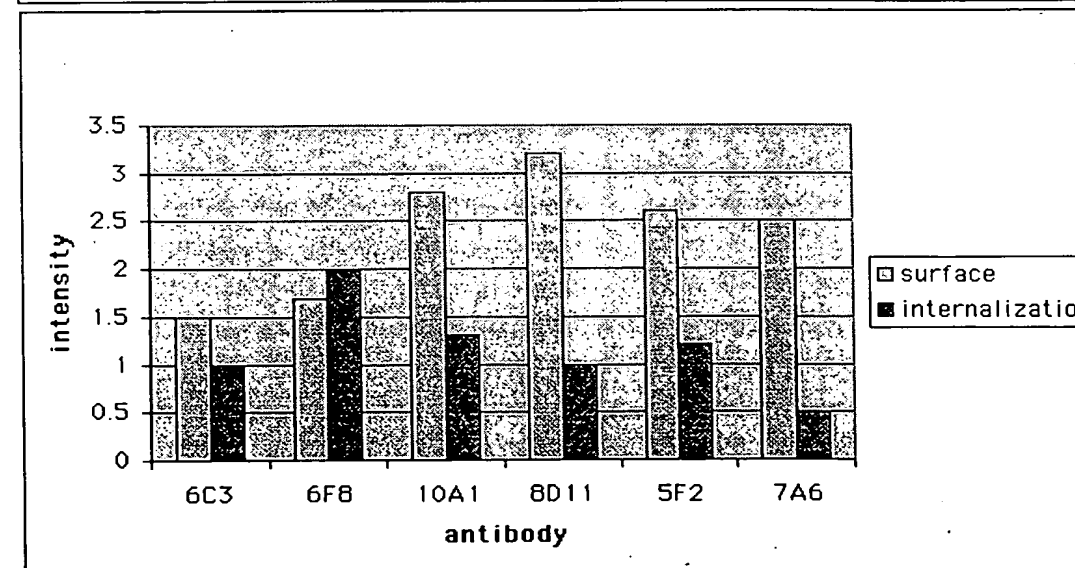


Fig. 7

FIG. 8A

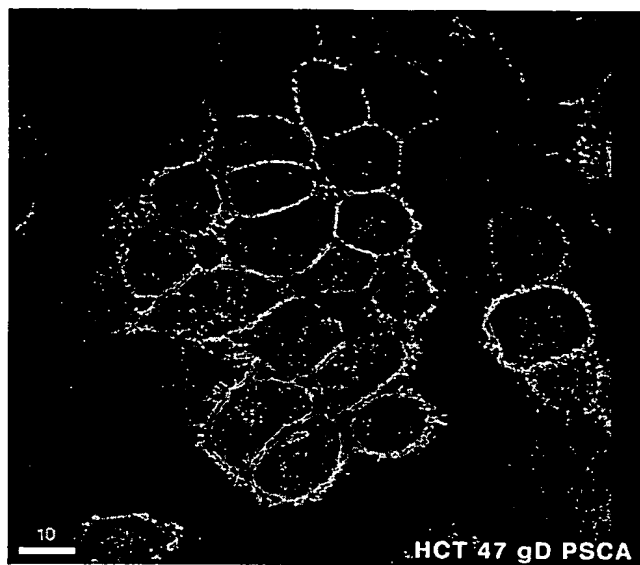


FIG. 8B

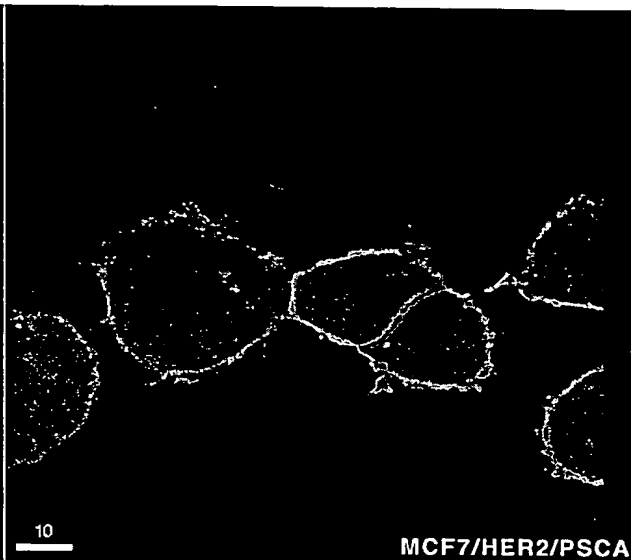


FIG. 8C

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FIG. 9A

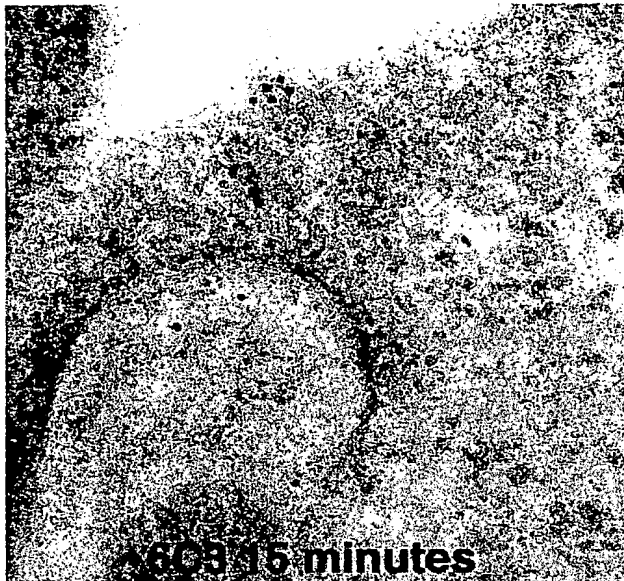


FIG. 9B

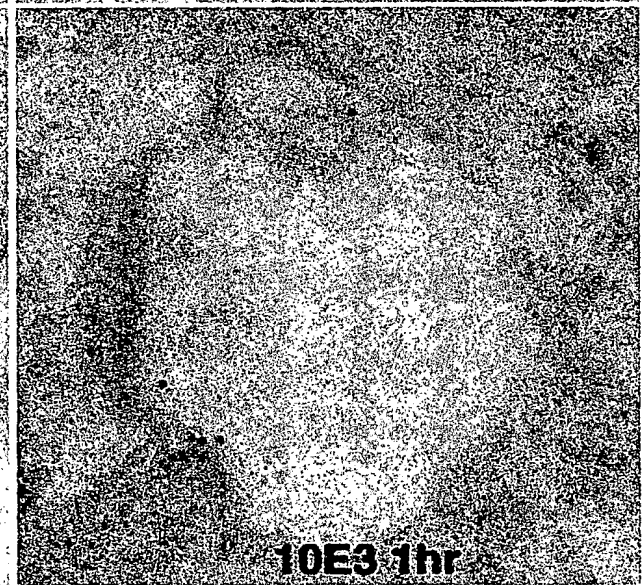
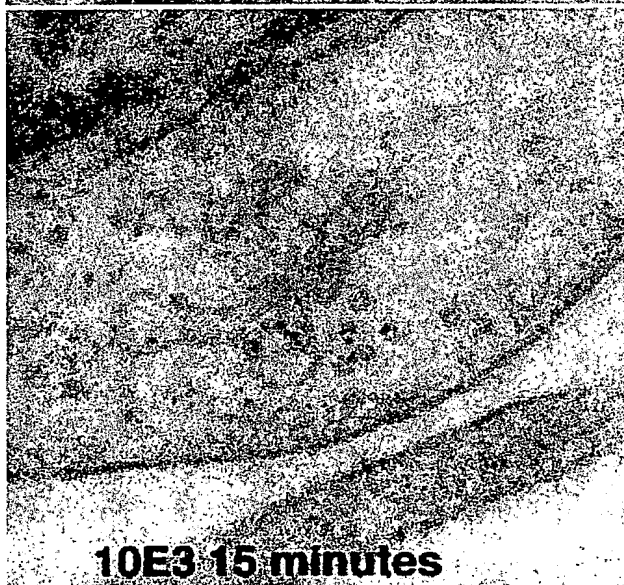
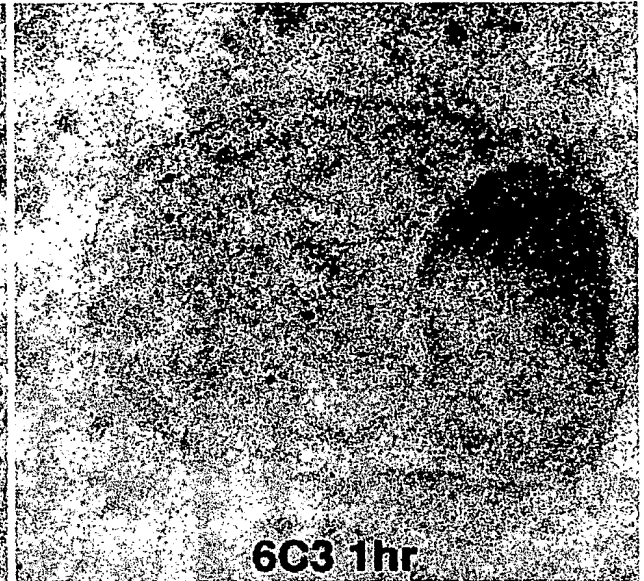


FIG. 9C

FIG. 9D

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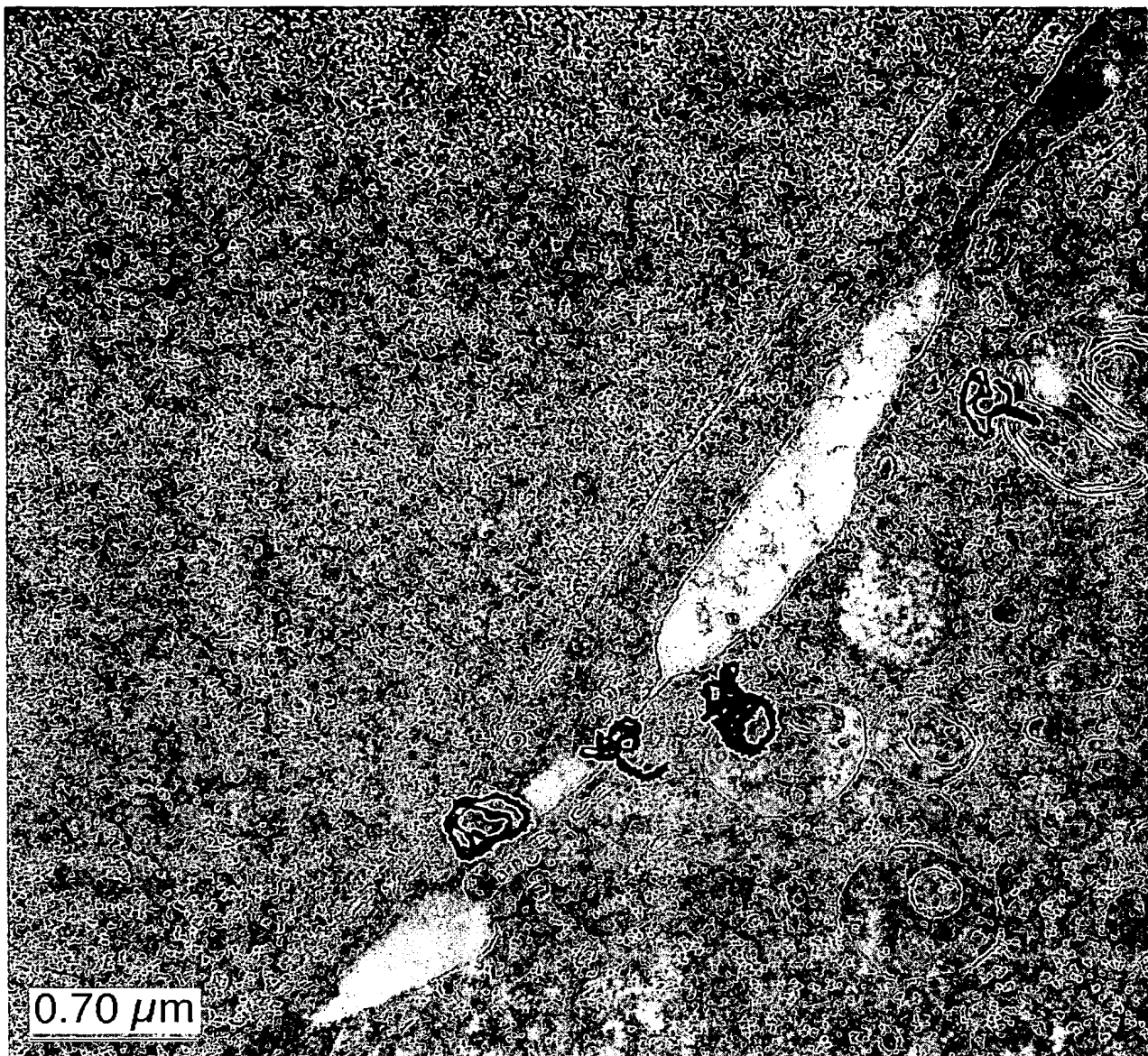


FIG. 10

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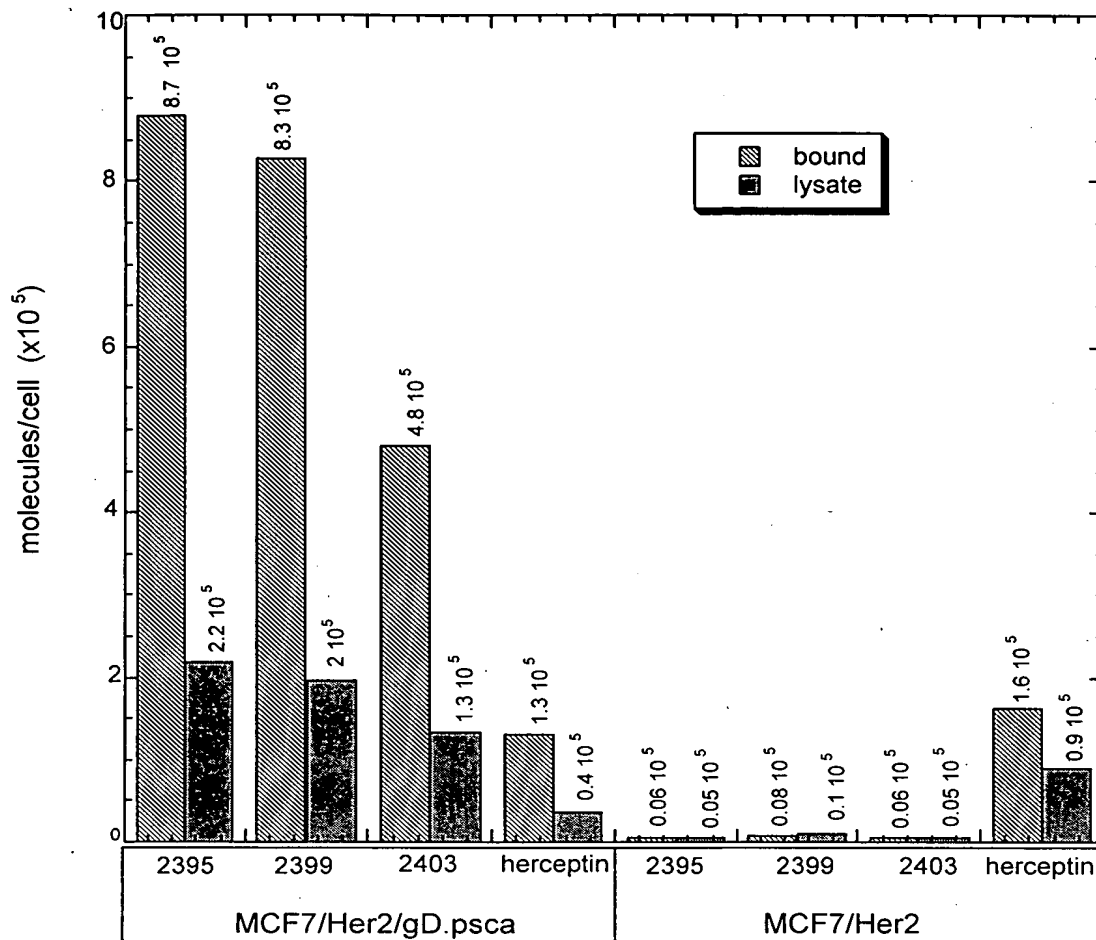


FIG. 11

chimeric 2403 (5F2.4H4.1E3) Light Chain

signal peptide MGWSCILFLVATATGVHS

DIVMTQAAPSVPTGESVSISCRSSKSLHNGNTYLYWFLQRPQSPQLLIYRMSNLASGVDPDRFSGSGGTAFILRISRVEAEDVG
VYYCLQHLEYPYTFGGGKLELK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

chimeric 2403 (5F2.4H4.1E3) IgG Heavy Chain

signal peptide MGWSCILFLVATATGVHS

QVQVQQPGAELVKPGAPVKLSCKASGYTFTNYWLNWVKQRPGRGLEWIGRIDPSDSEIHVDQKFKDKATLTVDKSSSTAYIQLSSLT
SEDSAVYYCALTGIYAMAYWGQTSVTSSAKTTG/PSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVTVPSSSLGTQYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVQLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYIT
LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEALHNHYT
QKLSLSLSPGK

chimeric 2761 (6B8.1D7.2B3) Fab - Light Chain

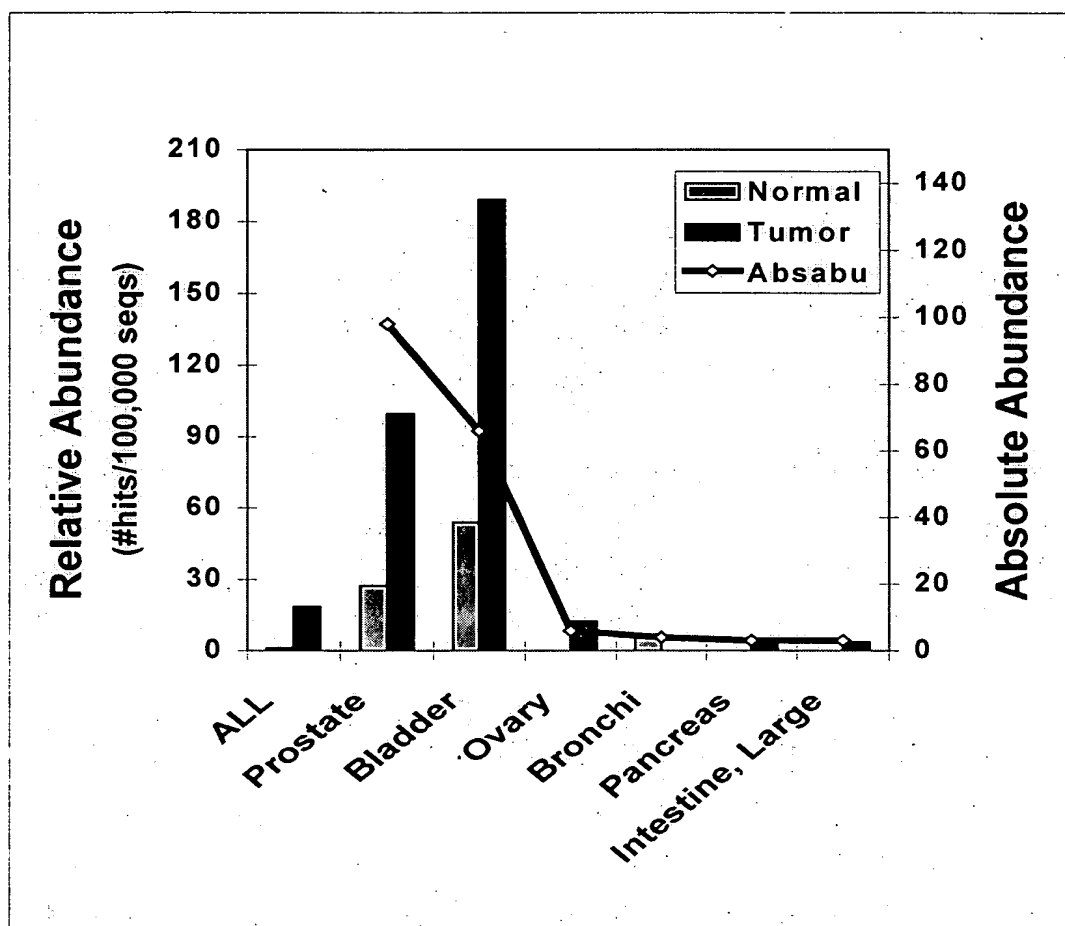
DVVMQTQPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNLWLLQRPQGSPKRLIYLVSTLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGV
YYCWQGTHTFPRTFGGGKLEIKR [V_L/C_κ junction]
TVAAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACET
HQGLSSPVTKSFNRGEC

chimeric 2761 (6B8.1D7.2B3) Fab - Heavy chain

EVQLQQSGPDLEKPGASVKISCKPSGNSFTGYYYIHVVVKQSHGKSLEWIGRVDPNNGFTSYNQKFKGKAILTVDKSSSTAYMELRSLTSE
DSA VYYCVGNFFDSWGQGTTLTVSSA [V_H/C_γ1 junction]
KTTGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSN
TKVDKKVEPKSCDKTHT

FIG. 13

FIG. 14



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1 ATGAAGGCTG TGCTGCTTGC CCTGTTGATG GCAGGCTTGG CCCTGCAGCC AGGCACTGCC
TACTTCCGAC ACGACGAACG GGACAACCTAC CGTCCGAACC GGGACGTCGG TCCGTGACGG
1 M K A V L L A L L M A G L A L Q P G T A

61 CTGCTGTGCT ACTCCTGCAA GGCCCAAGTG AGCAACGAGG ACTGCCTGAA TGTGGAGAAC
GACGACACGA TGAGGACGTT CCGGGTCCAC TCGTTGCTCC TGACGGACTT ACACCTCTTG
21 L L C Y S C K A Q V S N E D C L N V E N

121 TGCACGCAGC CGGAGGAGCA GTGCTGGACC GAGCGCATCC GCGCCGTGGG CCTCCTGACC
ACGTGCGTCG GCCTCCTCGT CACGACCTGG CTCGCGTAGG CGCGGCACCC GGAGGACTGG
41 C T Q P E E Q C W T E R I R A V G L L T

181 GTCATCAGCA AAGGCTGCAG CTCAAACTGC GTGGATGACT CACAGGACTA CTACGTGGGC
CAGTAGTCGT TTCCGACGTC GAGTTTGACG CACCTACTGA GTGTCTGAT GATGCACCCG
61 V I S K G C S S N C V D D S Q D Y Y V G

241 AAGAAGAACA TCACCTGCTG TGACACCGAC TTGTGCAACG CCAGCGGGGC CCATGCACCTG
TTCTTCTTGT AGTGGACGAC ACTGTGGCTG AACACGTTGC GGTGCCCCCG GGTACGTGAC
81 K K N I T C C D T D L C N A S G A H A L

301 CAGCCGGCTG CTGCCATCCT GGCACCTGCTC CCTGCACTCA GTCTGCTGCT TTGGAGCCCC
GTCGCGCCGAC GACGGTAGGA CCGTGACGAG GGACGTGAGT CAGACGACGA AACCTCGGGG
101 Q P A A A I L A L L P A L S L L L W S P

361 AGACAGCTGT AG
TCTGTCGACA TC
121 R Q L O

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FIG. 15

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1 ATGAAGGCTG TGCTGCTTGC CCTGTTGATG GCAGGCTTGG CCCTGCAGCC AGGCACTGCC
TACTTCCGAC ACGACGAACG GGACAACCTAC CGTCCGAACC GGGACGTCGG TCCGTGACGG
1 M K A V L L A L L M A G L A L Q P G T A

61 CTGTTGTGCT ACTCCTGCAA GGCCCAAGTG AGCAACGAGG ACTGCCTGAA TGTGGAGAAC
GACAACACGA TGAGGACGTT CCGGGTCCAC TCGTTGCTCC TGACGGACTT ACACCTCTTG
21 L L C Y S C K A Q V S N E D C L N V E N

121 TGCACGCAGC CGGAGGAGCA GTGCTGGACC GAGCGCATCC GCGCCGTGGG CCTCCTGACC
ACGTGCGTCG GCCTCCTCGT CACGACCTGG CTCGCGTAGG CGCGGCACCC GGAGGACTGG
41 C T Q P E E Q C W T E R I R A V G L L T

181 GTCATCAGCA AAGGCTGCAG CTCAAACTGC GTGGATGACT CACAGGACTA CTACGTGGGC
CAGTAGTCGT TTCCGACGTC GAGTTTGACG CACCTACTGA GTGTCTGAT GATGCACCCG
61 V I S K G C S S N C V D D S Q D Y Y V G

241 AAGAAGAACA TCACCTGCTG TGACACCGAC TTGTGCAACG CCAGCGGGGC CCATGCACCTG
TTCTTCTTGT AGTGGACGAC ACTGTGGCTG AACACGTTGC GGTGCCCCCG GGTACGGGAC
81 K K N I T C C D T D L C N A S G A H A L

301 CAGCCAGCTG CTGCCATCCT GGCACCTGCTC CCTGCACTCA GCCTGCTGCT TTGGGGCCCC
GTCGCTCGAC GACGGTAGGA CCGTGACGAG GGACGTGAGT CCGACGACGA AACCCCGGGG
101 Q P A A A I L A L L P A L S L L L W G P

361 AGACAGCTGT AG
TCTGTCGACA TC
121 R Q L O

```

FIG. 16

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	10	20	30	40	50
human	MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDECLQVENCTQLGEQCWT				

cynomolgus	MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDECLNVENCTQPEEQCWT				
	10	20	30	40	50
	60	70	80	90	100
human	ARIRAVGLLTVISKGCSLNCVDDSQDYVVGKKNITCCDIDLNASGAHAL				

cynomolgus	ERIRAVGLLTVISKGCSSNCVDDSQDYVVGKKNITCCDIDLNASGAHAL				
	60	70	80	90	100
	110	120			
human	QPAAAILALLPALGLLWGPGL				

cynomolgus	QPAAAILALLPALSLLLWSPRQL				
	110	120			

FIG. 17

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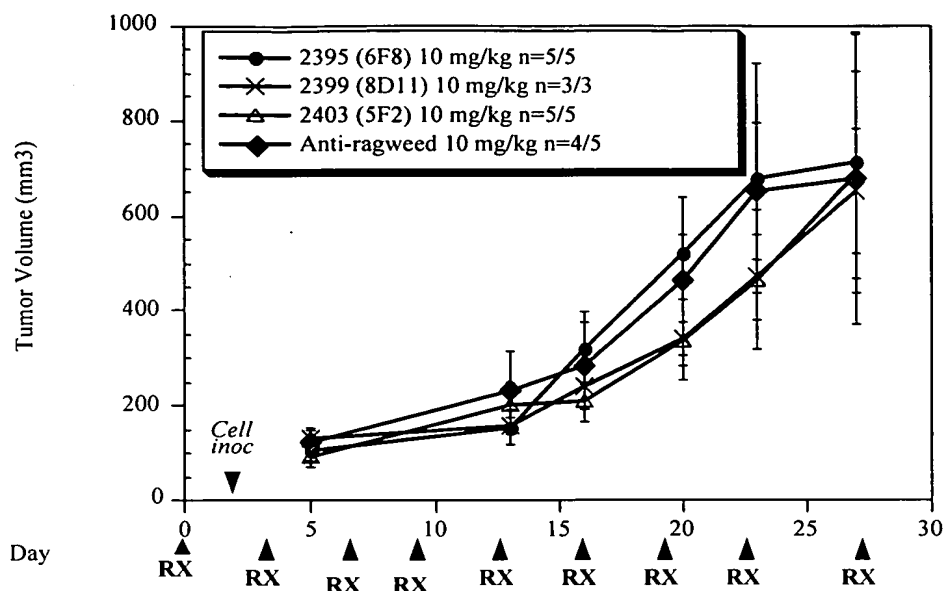


FIG. 18

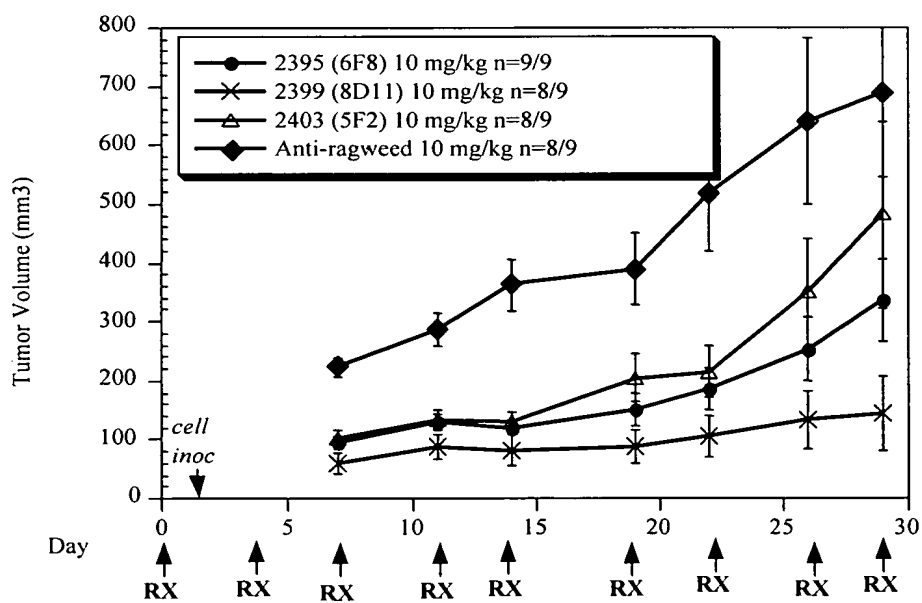


FIG. 19

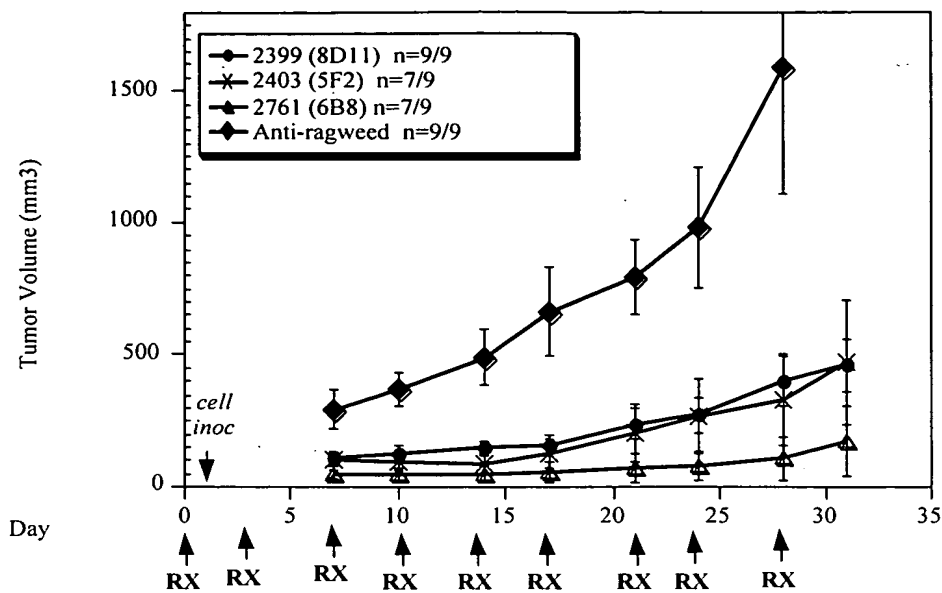


FIG. 20

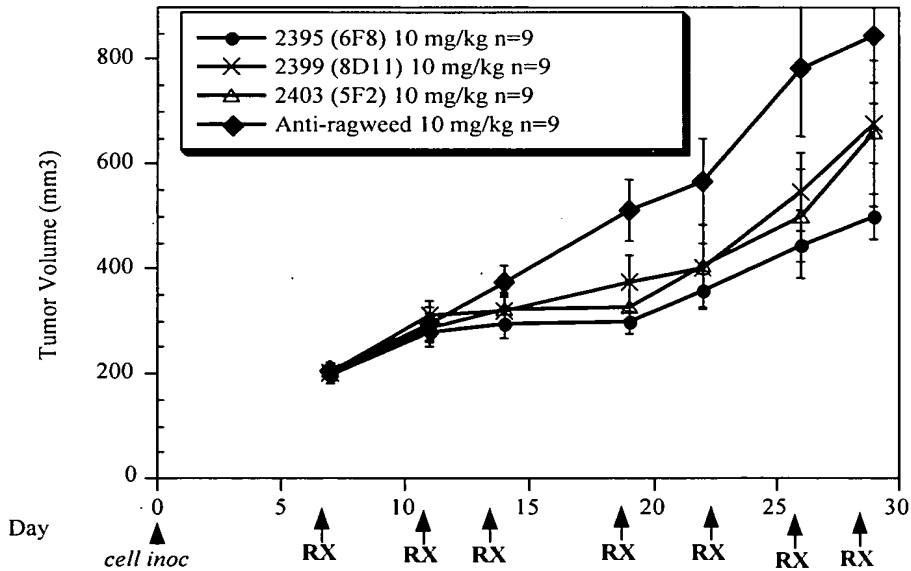


FIG. 21

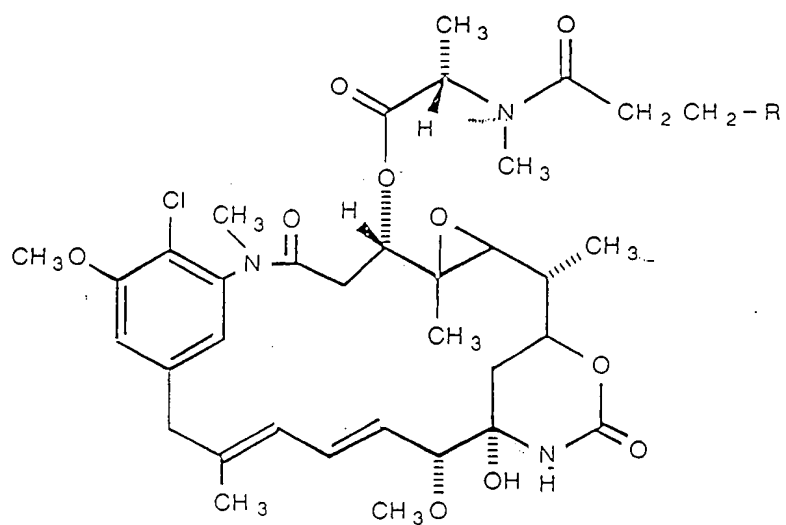


FIG. 22

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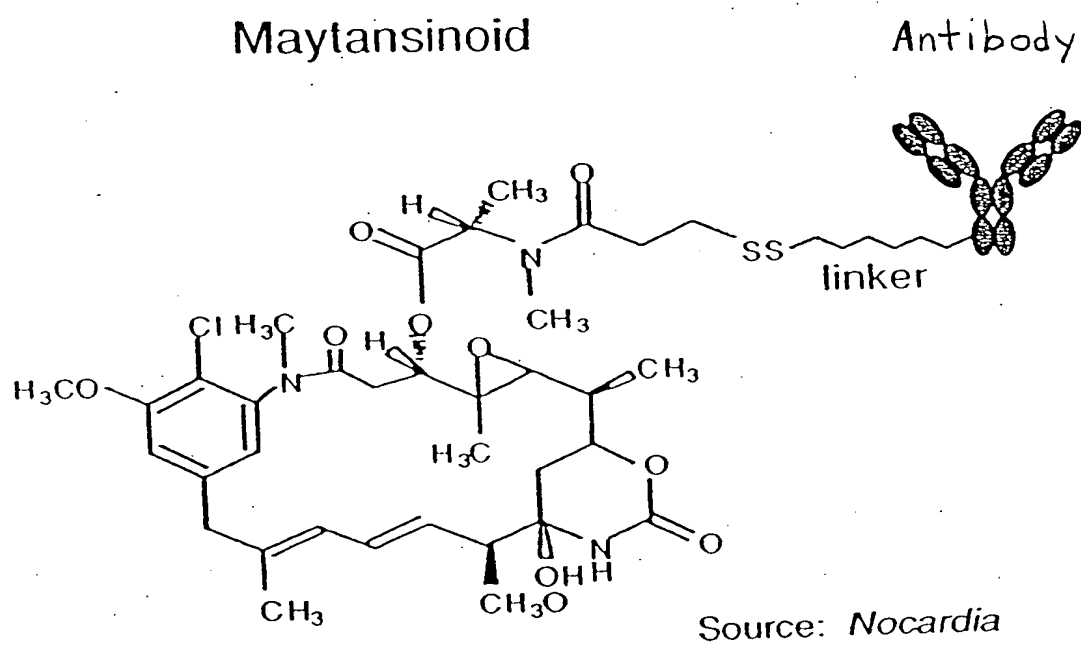


FIG. 23

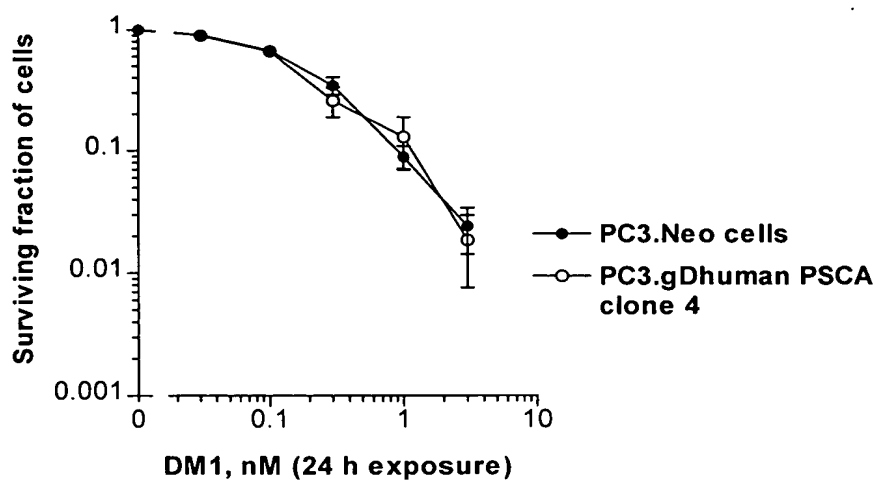


FIG. 24

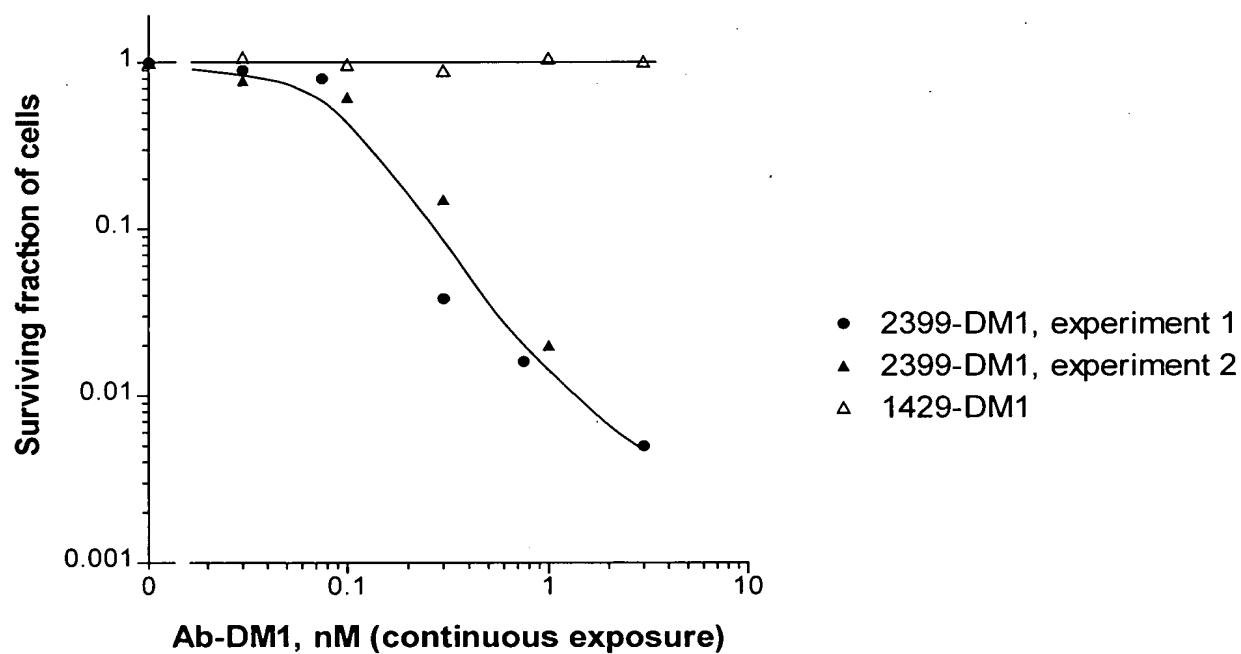


FIG. 25

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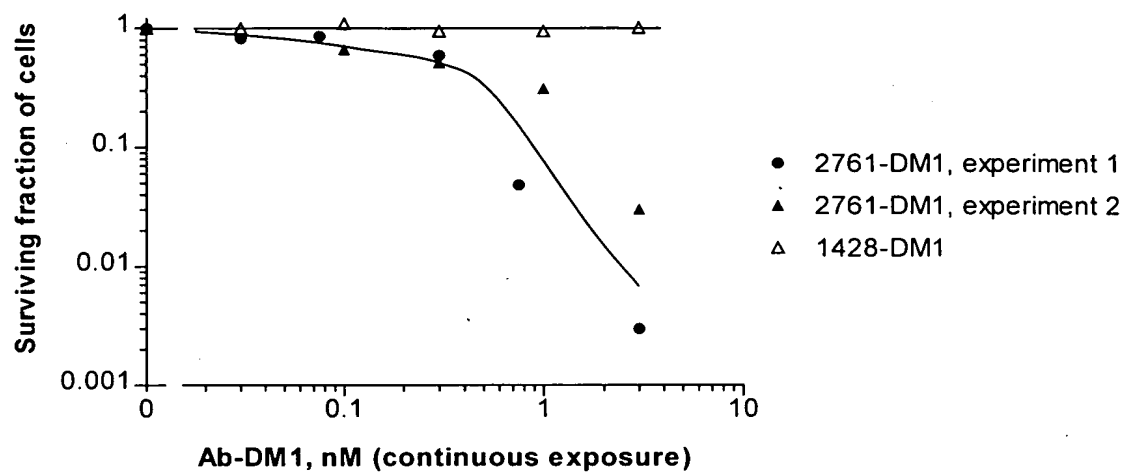


FIG. 26

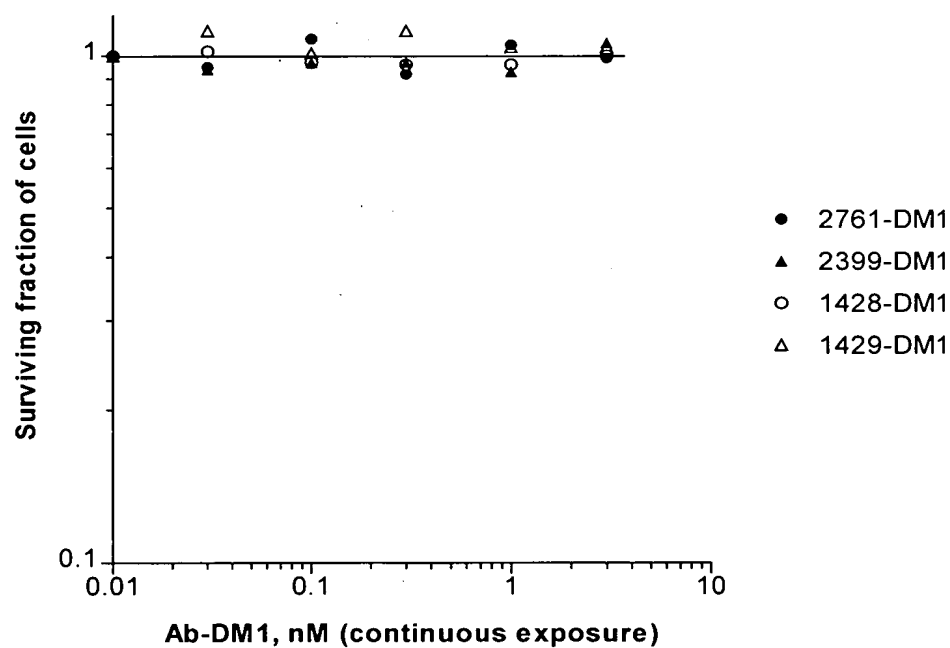


FIG. 27

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FIG. 28

